<!--StartFragment-->RESULT 1
ADC00348
ID ADC00348 standard; protein; 441 AA. APPENDIX B SEQ ID NO; 24
XX
AC ADC00348;
XX
DT 15-JUN-2007 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 393.
XX
KW enterohaemorragic; anti-bacterial; BOND_PC; hypothetical protein;
KW hypothetical protein ECs1812 [Escherichia coli O157:H7];
KW hypothetical protein ECs1812 [Escherichia coli O157:H7 str. Sakai];
KW unknown protein encoded by cryptic prophage CP-933P;
KW hypothetical protein [Escherichia coli O157:H7 str. Sakai].
XX
OS Escherichia coli; 0157:H7.
XX
PN JP2002355074-A.
XX
PD 10-DEC-2002.
XX
PF 24-JAN-2002; 2002JP-00015959.
XX
PR 24-JAN-2001; 2001JP-00112010.
XX
PA (UYTS-) UNIV TSUKUBA.
XX
DR WPI; 2003-451640/43.
DR PC:NCBI; gi13259568.
XX
PT Enterohemorragic Escherichia coli O157:H7-specific nucleic acid molecule
PT and a polypeptide and its use, a polypeptide, a vector and a host cell.
XX
PS Claim 3; SEQ ID NO 393; 2067pp; Japanese.
XX
CC The invention relates to a novel enterohaemorragic Escherichia coli
CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC has anti-bacterial activity. The polypeptide can be used in detection
CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC genome of Enterohaemorragic E coli O157:H7 was determined. The present
CC sequence represents an E. coli 0157:H7-specific polypeptide of the
CC invention.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 441 AA;

  Query Match 100.0%; Score 2341; DB 6; Length 441;
  Best Local Similarity 100.0%; Pred. No. 1.1e-197;
  Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVVNIPDDIQQHAPECGET 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVVNIPDDIQQHAPECGET 60

Qy         61 TALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISGKY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISGKY 120

Qy        121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIAST 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIAST 180

Qy        181 GTSATTSTVTTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY 240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTSATTSTVTTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY 240

Qy        241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLDNPNTKYAVLTNAAANALGALGGF 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLDNPNTKYAVLTNAAANALGALGGF 300

Qy        301 AVSRFASTDPMLSPHIGAMVGQAAGHAIQYNTPGLKPDTILWWAGATLGAADLNKAEFEV 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AVSRFASTDPMLSPHIGAMVGQAAGHAIQYNTPGLKPDTILWWAGATLGAADLNKAEFEV 360

Qy        361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420

Qy        421 LPHHNPSNHVDIFDIIQETRV 441
                |||||||||||||||||||||
Db        421 LPHHNPSNHVDIFDIIQETRV 441
<!--EndFragment-->
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